



SEQUENCE LISTING

<110> Lipton, Stuart A.
Okamoto, Shu-ichi

<120> Methods of Differentiating and
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> 66654-622

<140> US 09/876,187

<141> 2001-06-05

<150> US 60/209,539

<151> 2000-06-05

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<213> Homo sapiens

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tggccaggct ggtctcgaac tctggacctc agatcttgta gaaaatttca gctgtagccc 300
ttggactaga agctgaaata acagaagctg tgtacgatgc attaggggtat tgaagaaaat 360
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Met
1
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Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
20 25 30
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gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
35 40 45
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agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa gtt 609
Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val
50 55 60 65
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Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn	
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tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac	705
Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
85 90 95	
agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa	753
Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
100 105 110	
aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
115 120 125	
aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
130 135 140 145	
gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt	897
Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
150 155 160	
tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca	945
Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
165 170 175	
agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct	993
Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
180 185 190	
gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg	1041
Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
195 200 205	
agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca gtg	1089
Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
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Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
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Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro	
245 250 255	
cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt	1233
Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu	
260 265 270	
cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg	1281
Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
275 280 285	

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Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln	
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Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser	
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ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac aac	1425
Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn	
325 330 335	
act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc	1473
Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe	
340 345 350	
aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag cag	1521
Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln	
355 360 365	
cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg cag	1569
His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln	
370 375 380 385	
tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc	1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser	
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atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg	1665
Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser	
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ggc ttc cag cag cag cag cag cag cag cag cag cag cag ccg ccg cca	1713
Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro	
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Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln Glu	
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Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Tyr	
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gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca att	1857
Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile	
470 475 480	
gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct gta	1905
Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val	
485 490 495	
aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt	1955
Lys Arg Met Arg Met Asp Ala Trp Val Thr	
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<212> PRT

<213> Homo sapiens

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
35          40          45
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
50          55          60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
65          70          75          80
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
85          90          95
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
100         105         110
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
115         120         125
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
130         135         140
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
145         150         155         160
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
165         170         175
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
180         185         190
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
195         200         205
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
210         215         220
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
225         230         235         240
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
245         250         255
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp

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Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro		
305	310	315
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr		
325	330	335
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly		
340	345	350
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln		
355	360	365
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly		
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Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile		
385	390	395
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro		
405	410	415
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro		
420	425	430
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln		
435	440	445
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser		
450	455	460
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro		
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 <222> (443)...(1537)

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 cctcagcctg atcctggaag agactcgggg cccccagcc tccgccaacc cagacaaaga 420
 tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
 1 5 10
 atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
 Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
 15 20 25

ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag	568
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu	
30 35 40	
ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc	616
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala	
45 50 55	
agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag	664
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu	
60 65 70	
ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg	712
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg	
75 80 85 90	
agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct	760
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro	
95 100 105	
gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat	808
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp	
110 115 120	
ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc	856
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro	
125 130 135	
agc cca gat gtg gta tac ggg gcc tta ccg cca cca ggc tgt gac ccc	904
Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro	
140 145 150	
agt ggg ctt ggg gaa gca ctg ccc gcc cag agc cgc cca tct ccc ttc	952
Ser Gly Leu Gly Glu Ala Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe	
155 160 165 170	
cga cca gca gcc ccc aaa gcc ggg ccc cca ggc ctg gtg cac cct ctc	1000
Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu	
175 180 185	
ttc tca cca agc cac ctc acc agc aag aca cca ccc cca ctg tac ctg	1048
Phe Ser Pro Ser His Leu Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu	
190 195 200	
ccg acg gaa ggg cgg agg tca gac ctg cct ggt ggc ctg gct ggg ccc	1096
Pro Thr Glu Gly Arg Arg Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro	
205 210 215	
cga ggg gga cta aac acc tcc aga agc ctc tac agt ggc ctg cag aac	1144
Arg Gly Gly Leu Asn Thr Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn	
220 225 230	
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235 240 245 250	

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ctc ccc gga ggc ccc cca gtg ggg gcc gaa gcc tgg gcg agg agg gtc 1240
Leu Pro Gly Gly Pro Pro Val Gly Ala Glu Ala Trp Ala Arg Arg Val
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Pro Gln Pro Ala Ala Pro Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser
                270                275                280

ctg agc gcc tct ctc cgg ccc ccg ggg gcc ccg gcg act ttc cta aga 1336
Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg
                285                290                295

cct tcc cct atc cct tgc tcc tcg ccc ggt ccc tgg cag agc ctc tgc 1384
Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys
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ggc ctg ggc ccg ccc tgc gcc ggc tgc cct tgg ccg acg gct ggc ccc 1432
Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro
315                320                325                330

ggt agg aga tca ccc ggt ggc acc agc cca gag cgc tcg cca ggt acg 1480
Gly Arg Arg Ser Pro Gly Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr
                335                340                345

gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag 1528
Ala Arg Ala Arg Gly Asp Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys
                350                355                360

acc caa cag tgacgcccc ctccgcggtg ggggcttgga ggtgggcggc 1577
Thr Gln Gln
                365

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<210> 4
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 <212> PRT
 <213> Homo sapiens

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35      40      45
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50      55      60
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65      70      75      80
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
 85      90      95
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
100     105     110
Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro
115     120     125

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Leu	Pro	Ala	Gln	Ser	Arg	Pro	Ser	Pro	Phe	Arg	Pro	Ala	Ala	Pro	Lys
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Ala	Gly	Pro	Pro	Gly	Leu	Val	His	Pro	Leu	Phe	Ser	Pro	Ser	His	Leu
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Thr	Ser	Lys	Thr	Pro	Pro	Pro	Leu	Tyr	Leu	Pro	Thr	Glu	Gly	Arg	Arg
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Ser	Asp	Leu	Pro	Gly	Gly	Leu	Ala	Gly	Pro	Arg	Gly	Gly	Leu	Asn	Thr
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Pro	Gly	Pro	Pro	Leu	Gly	Ser	Phe	Pro	Phe	Leu	Pro	Gly	Gly	Pro	Pro
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Pro	Arg	Arg	Pro	Pro	Gln	Ser	Ala	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Arg
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Ala	Gly	Cys	Pro	Trp	Pro	Thr	Ala	Gly	Pro	Gly	Arg	Arg	Ser	Pro	Gly
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Gly	Thr	Ser	Pro	Glu	Arg	Ser	Pro	Gly	Thr	Ala	Arg	Ala	Arg	Gly	Asp
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 <222> (402)...(1820)

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 Met Gly Arg Lys Lys
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att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt 464
 Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
 10 15 20

aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg 512

Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala	Tyr	Glu	Leu	Ser	Val	
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Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	Asn	Ser	Thr	Asn	Lys	
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Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr	Asn	Ser	Asp	Ile	Val	
70					75				80					85		
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Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys	Asp	Ser	Pro	Asp	Pro	
			90					95					100			
gat	gcg	gac	gat	tcc	gta	ggc	cac	agc	cct	gag	tct	gag	gac	aag	tac	752
Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu	Ser	Glu	Asp	Lys	Tyr	
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agg	aaa	att	aac	gaa	gat	att	gat	cta	atg	atc	agc	agg	caa	aga	ttg	800
Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile	Ser	Arg	Gln	Arg	Leu	
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tgt	gct	gtt	cca	cct	ccc	aac	ttc	gag	atg	cca	gtc	tcc	atc	cca	gtg	848
Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro	Val	Ser	Ile	Pro	Val	
	135					140					145					
tcc	agc	cac	aac	agt	ttg	gtg	tac	agc	aac	cct	gtc	agc	tca	ctg	gga	896
Ser	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro	Val	Ser	Ser	Leu	Gly	
150					155				160					165		
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Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser	Leu	Gln	Arg	Asn	Ser	
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Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser	Ala	Gly	Asn	Thr	Gly	
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Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala	Gly	Thr	Ser	Ala	Gly	
	200					205						210				
aac	ggg	tat	ggc	aat	ccc	cga	aac	tca	cca	ggc	ctg	ctg	gtc	tca	cct	1088
Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly	Leu	Leu	Val	Ser	Pro	
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ggc	aac	ttg	aac	aag	aat	atg	caa	gca	aaa	tct	cct	ccc	cca	atg	aat	1136
Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser	Pro	Pro	Pro	Met	Asn	
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Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu Asp Val Asp Leu Leu	
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Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr	
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cca gtg gtt tcc gta gca act cct act tta cca gga caa gga atg gga	1328
Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly	
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Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu	
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Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala	
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Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His	
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Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn	
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Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro	
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<212> PRT

<213> Homo sapiens

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Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
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Cys	Thr	Ser	Thr	His	Leu	Ser	Gln	Ser	Ser	Asn	Leu	Ser	Leu	Pro	Ser	
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Thr	Gln	Ser	Leu	Asn	Ile	Lys	Ser	Glu	Pro	Val	Ser	Pro	Pro	Arg	Asp	
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Gly	Ser	Asp	Arg	Glu	Asp	His	Arg	Asn	Glu	Phe	His	Ser	Pro	Ile	Gly	
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Leu	Thr	Arg	Pro	Ser	Pro	Asp	Glu	Arg	Glu	Ser	Pro	Ser	Val	Lys	Arg	
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<210> 7

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (196)...(1761)

<400> 7

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Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr
1 5 10

gac gag cgg aac cga cag gtg act ttc acc aag cgg aag ttt ggc ctg 279
Asp Glu Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu
15 20 25

atg aag aag gcg tat gag ctg agc gtg cta tgt gac tgc gag atc gca 327
Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala
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ctc atc atc ttc aac cac tcc aac aag ctg ttc cag tac gcc agc acc 375
Leu Ile Ile Phe Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr
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gac atg gac aag gtg ctg ctc aag tac acg gag tac aat gag cca cac 423
Asp Met Asp Lys Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His
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gag agc cgc acc aac gcc gac atc atc gag acc ctg agg aag aag ggc 471
Glu Ser Arg Thr Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly
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Phe Asn Gly Cys Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu
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Gln Ser Pro Leu Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu
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gac ggg ctc ttc cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt 615
Asp Gly Leu Phe Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe
125 130 135 140

gcc atg cct gtc acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc 663
Ala Met Pro Val Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe
145 150 155

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160 165 170

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Leu Thr Asp Pro Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg
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Met	Leu	Gly	Gly	Asp	Leu	Asn	Ser	Ala	Asn	Gly	Ala	Cys	Pro	Ser	Pro		
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Val	Gly	Asn	Gly	Tyr	Val	Ser	Ala	Arg	Ala	Ser	Pro	Gly	Leu	Leu	Pro		
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gtg	gcc	aat	ggc	aac	agc	cta	aac	aag	gtc	atc	cct	gcc	aag	tct	ccg	951	
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Pro	Pro	Pro	Thr	His	Ser	Thr	Gln	Leu	Gly	Ala	Pro	Ser	Arg	Lys	Pro		
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ccg	caa	cag	cca	cct	cag	caa	cag	tcc	cac	ctg	gtc	cct	gta	tct	ctc	1431	
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cca agc cgt gag cgc agc cct gcg cct ccc cct cca gct gtg ttc cca			1575
Pro Ser Arg Glu Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro			
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Ala Ala Arg Pro Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly			
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Ser Tyr Glu Thr Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro			
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Thr Leu Gly Leu Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser			
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<211> 521

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His	Ser	Thr	Gln	Leu	Gly	Ala	Pro	Ser	Arg	Lys	Pro	Asp	Leu	Arg	Val
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Ile	Thr	Ser	Gln	Ala	Gly	Lys	Gly	Leu	Met	His	His	Leu	Thr	Glu	Asp
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Pro	Gln	Gln	Gln	Ser	His	Leu	Val	Pro	Val	Ser	Leu	Ser	Asn	Leu	Ile
				405					410					415	
Pro	Gly	Ser	Pro	Leu	Pro	His	Val	Gly	Ala	Ala	Leu	Thr	Val	Thr	Thr
			420					425					430		
His	Pro	His	Ile	Ser	Ile	Lys	Ser	Glu	Pro	Val	Ser	Pro	Ser	Arg	Glu
		435					440					445			
Arg	Ser	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Val	Phe	Pro	Ala	Ala	Arg	Pro
		450				455					460				
Glu	Pro	Gly	Asp	Gly	Leu	Ser	Ser	Pro	Ala	Gly	Gly	Ser	Tyr	Glu	Thr
465					470					475					480
Gly	Asp	Arg	Asp	Asp	Gly	Arg	Gly	Asp	Phe	Gly	Pro	Thr	Leu	Gly	Leu
				485					490					495	
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